Supplemental Figure 1: Distribution of the number of non-duplicate aligned reads per sample.

Supplemental Figure 2: FF distributions for each bioinformatics tool, separated for male (blue) and female (salmon) fetuses. DEFRAG is based on Y chromosome analysis and therefore does not include FF for female fetuses.

Supplemental Figure 3: FF as a function of blood shipping time (A-male fetuses with DEFRAG_W, B-female fetuses with SeqFF).

Supplemental Figure 4: Distribution of gestational age in this cohort.

Supplemental Figure 5: Female fetuses FF as determined by SeqFF as a function of gestational time (A), maternal age (B), weight (C), and trisomies (D).

Supplemental Figure 6: FF as a function of BMI (A-male fetuses with DEFRAG_W, B-female fetuses with SeqFF).